

SEQUENCE LISTING

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<120> Tereuin C-Terminal Associated Peptides (TCAP) And Methods And Uses
Thereof

<130> 2223-189

<140>

<141>

<150> US 60/376,879

<151> 2002-05-02

<150> US 60/377,231

<151> 2002-05-03

<150> US 60/424,016

<151> 2002-11-06

<160> 136

<170> PatentIn version 3.1

<210> 1

<211> 1490

<212> DNA

<213> Artificial Sequence

<220>

<223> Rainbow Trout Ten M3 carboxy termini'

<400> 1

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gtggtcacca	acgctctgaa	catcgccaac	gaggactgca	tcaaggtcgc	cgccgtcctc	240
aacaatgcgt	tctacctgga	ggacctgcac	ttcacggtgg	agggacgcga	cacgcactac	300
ttcatcaaga	ccagcctccc	ggagagcgac	ctgggagcgc	tgaggctgac	aagcgggagg	360
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agtaaaatgt	agaatatctt	aaactgaact	atacctaata	ctaccactgt	ggggcctgaa	960
aatcaaacia	aacggctcca	actgacgcaa	atgtttgtcc	catgtgctat	acagcgttga	1020
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ggagaaaaaa	acgttttttt	tttttttaaa	tagacttcct	gaatttgctt	tcggaaaaaa	1140
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taatagaaga	aaagccttct	ggtttcttac	acaggacaac	gtctataatc	tgattctaca	1260
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cttgcttggt	cttctgcttt	tctttccaaa	agggacaaaa	cagctcccac	caagtgactt	1440
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<210> 2

<211> 756

<212> DNA

<213> Artificial Sequence

<220>

<223> Rainbow Trout Ten M3 coding sequence of carboxy termini of Ten M3

<400> 2

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aggatgccgg agatccagct gagccgccgg cgctccaacc gggagaaacc ctggctgtgg	120
ttcgccaccg ccaagtctct gatcggtaag ggtgtcatgt tggcggtgac gcagggccgt	180
gtggtcacca acgctctgaa catcgccaac gaggactgca tcaaggtcgc cgccgtcctc	240
aacaatgcgt tctacctgga ggacctgcac ttcacggtgg agggacgcga cacgcactac	300
ttcatcaaga ccagcctccc ggagagcgac ctgggagcgc tgaggctgac aagcgggagg	360
aagtcgctgg agaacggaag tcaacgtgac tgtgtcccag tccaccaccg tggatgaacgg	420
cagaaccggc gcttcgccga cgtggagctg cagtacggcg ctctagcgct ccacgtgcgc	480
tatggcatga ctctggacga ggagaaggcg cgtgtgctgg agcaggccag gcagaaggcg	540
ttgtcgagtg cctgggtccag ggagcaacaa cgggtgaggg agggggagga ggggggtgagg	600
ctgtggacgg agggggagaa gaggcagctg ctgagcggga ggaagggttct gggctacgac	660
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<210> 3

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> Rainbow Trout Ten M3 carboxy termini of Ten M3

<400> 3

Ser	Ile	Ser	Gly	Val	Gln	Gln	Glu	Val	Thr	Arg	Gln	Ala	Lys	Ala	Phe
1				5					10					15	

Leu Ser Phe Glu Arg Met Pro Glu Ile Gln Leu Ser Arg Arg Arg Ser
20 25 30

Asn Arg Glu Lys Pro Trp Leu Trp Phe Ala Thr Ala Lys Ser Leu Ile
35 40 45

Gly Lys Gly Val Met Leu Ala Val Thr Gln Gly Arg Val Val Thr Asn
50 55 60

Ala Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu
65 70 75 80

Asn Asn Ala Phe Tyr Leu Glu Asp Leu His Phe Thr Val Glu Gly Arg
85 90 95

Asp Thr His Tyr Phe Ile Lys Thr Ser Leu Pro Glu Ser Asp Leu Gly
100 105 110

Ala Leu Arg Leu Thr Ser Gly Arg Lys Ser Leu Glu Asn Gly Val Asn
115 120 125

Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg
130 135 140

Phe Ala Asp Val Glu Leu Gln Tyr Gly Ala Leu Ala Leu His Val Arg
145 150 155 160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Gln Ala
165 170 175

Arg Gln Lys Ala Leu Ser Ser Ala Trp Ser Arg Glu Gln Gln Arg Val
180 185 190

Arg Glu Gly Glu Glu Gly Val Arg Leu Trp Thr Glu Gly Glu Lys Arg
195 200 205

Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val
210 215 220

Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
225 230 235 240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg

245

250

<210> 4

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse Ten M1

<400> 4

Met Ile Leu Gly Ile Gln Cys Glu Leu Gln Lys Gln Leu Arg Asn Phe
1 5 10 15

Ile Ser Leu Asp Gln Leu Pro Met Thr Pro Gln Tyr Asn Glu Gly Arg
20 25 30

Cys Leu Glu Gly Gly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val
35 40 45

Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Glu Gly Ile Val Thr Ala
50 55 60

Asp Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile
65 70 75 80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly
85 90 95

Arg Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu
100 105 110

Val Leu Ile Gly Asn Thr Gly Gly Arg Arg Ile Leu Glu Asn Gly Val
115 120 125

Asn Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg
130 135 140

Arg Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile
145 150 155 160

Arg Tyr Gly Thr Thr Val Glu Glu Glu Lys Asn His Val Leu Glu Met
165 170 175

Ala Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Gln Glu Gln Arg Arg
180 185 190

Leu Gln Glu Gly Glu Glu Gly Thr Arg Val Trp Thr Glu Gly Glu Lys
195 200 205

Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
210 215 220

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
225 230 235 240

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
245 250

<210> 5

<211> 253

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse Ten M2

<400> 5

Leu Ile Thr Gly Val Gln Gln Thr Thr Glu Arg His Asn Gln Ala Phe
1 5 10 15

Leu Ala Leu Glu Gly Gln Val Ile Thr Lys Lys Leu His Ala Ser Ile
20 25 30

Arg Glu Lys Ala Gly His Trp Phe Ala Thr Thr Thr Pro Ile Ile Gly
35 40 45

Lys Gly Ile Met Phe Ala Ile Lys Glu Gly Arg Val Thr Thr Gly Val
50 55 60

Ser Ser Ile Ala Ser Glu Asp Ser Arg Lys Val Ala Ser Val Leu Asn
65 70 75 80

Asn Ala Tyr Tyr Leu Asp Lys Met His Tyr Ser Ile Glu Gly Lys Asp
85 90 95

Thr His Tyr Phe Val Lys Ile Gly Ala Ala Asp Gly Asp Leu Val Thr
100 105 110

Leu Gly Thr Thr Ile Gly Arg Lys Val Leu Glu Ser Gly Val Asn Val
115 120 125

Thr Val Ser Gln Pro Thr Leu Leu Val Asn Gly Arg Thr Arg Arg Phe
130 135 140

Thr Asn Ile Glu Phe Gln Tyr Ser Thr Leu Leu Leu Ser Ile Arg Tyr
145 150 155 160

Gly Leu Thr Pro Asp Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Asp
165 170 175

Gln Ala Gly Gln Arg Ala Leu Gly Thr Ala Trp Ala Lys Glu Gln Gln
180 185 190

Lys Ala Arg Asp Gly Arg Glu Gly Ser Arg Leu Trp Thr Glu Gly Glu
195 200 205

Lys Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr
210 215 220

Tyr Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser
225 230 235 240

Asn Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
245 250

<210> 6

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse Ten M3

<400> 6

Pro Ile Phe Gly Val Gln Gln Gln Val Ala Arg Gln Ala Lys Ala Phe
1 5 10 15

Leu Ser Leu Gly Lys Met Ala Glu Val Gln Val Ser Arg Arg Lys Ala
20 25 30

Gly Ala Glu Gln Ser Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile
35 40 45

Gly Lys Gly Val Met Leu Ala Val Ser Gln Gly Arg Val Gln Thr Asn
50 55 60

Val Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu
65 70 75 80

Asn Asn Ala Phe Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Lys
85 90 95

Asp Thr His Tyr Phe Ile Lys Thr Thr Thr Pro Glu Ser Asp Leu Gly
100 105 110

Thr Leu Arg Leu Thr Ser Gly Arg Lys Ala Leu Glu Asn Gly Ile Asn
115 120 125

Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg
130 135 140

Phe Ala Asp Val Glu Met Gln Phe Gly Ala Leu Ala Leu His Val Arg
145 150 155 160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Ile Leu Glu Gln Ala
165 170 175

Arg Gln Arg Ala Leu Ala Arg Ala Trp Ala Arg Glu Gln Gln Arg Val
180 185 190

Arg Asp Gly Glu Glu Gly Ala Arg Leu Trp Thr Glu Gly Glu Lys Arg
195 200 205

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
210 215 220

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile

225 230 235 240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
245 250

<210> 7

<211> 243

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Mouse Ten M4

<400> 7

Ser Ile Leu Gly Val Gln Cys Glu Val Gln Lys Gln Leu Lys Ala Phe
1 5 10 15

Val Thr Leu Glu Arg Phe Asp Gln Leu Tyr Gly Ser Thr Ile Thr Ser
20 25 30

Cys Gln Gln Ala Pro Glu Thr Lys Lys Phe Ala Ser Ser Gly Ser Ile
35 40 45

Phe Gly Lys Gly Val Lys Phe Ala Leu Lys Asp Gly Arg Val Thr Thr
50 55 60

Asp Ile Ile Ser Val Ala Asn Glu Asp Gly Arg Arg Ile Ala Ala Ile
65 70 75 80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Asp Gly
85 90 95

Val Asp Thr His Tyr Phe Val Lys Pro Gly Pro Ser Glu Gly Asp Leu
100 105 110

Ala Ile Leu Gly Leu Ser Gly Gly Arg Arg Thr Leu Glu Asn Gly Val
115 120 125

Asn Val Thr Val Ser Gln Ile Asn Thr Met Leu Ile Gln Leu Gln Tyr
130 135 140

Arg Ala Leu Cys Leu Asn Thr Arg Tyr Gly Thr Thr Val Asp Glu Glu
145 150 155 160

Lys Val Arg Val Leu Glu Leu Ala Arg Gln Arg Ala Val Arg Gln Ala
165 170 175

Trp Ala Arg Glu Gln Gln Arg Leu Arg Glu Gly Glu Glu Gly Leu Arg
180 185 190

Ala Trp Thr Asp Gly Glu Lys Gln Gln Val Leu Asn Thr Gly Arg Val
195 200 205

Gln Gly Tyr Asp Gly Phe Phe Val Thr Ser Val Glu Gln Tyr Pro Glu
210 215 220

Leu Ser Asp Ser Ala Asn Asn Ile His Phe Met Arg Gln Ser Glu Met
225 230 235 240

Gly Arg Arg

<210> 8

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Ten M1

<400> 8

Thr Ile Leu Gly Ile Gln Cys Glu Leu Gln Lys Gln Leu Arg Asn Phe
1 5 10 15

Ile Ser Leu Asp Gln Leu Pro Met Thr Pro Arg Tyr Asn Asp Gly Arg
20 25 30

Cys Leu Glu Gly Gly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val
35 40 45

Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Asp Gly Ile Val Thr Ala
50 55 60

Asp Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile
65 70 75 80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly
85 90 95

Arg Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu
100 105 110

Val Leu Ile Gly Asn Thr Gly Gly Arg Arg Ile Leu Glu Asn Gly Val
115 120 125

Asn Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg
130 135 140

Arg Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile
145 150 155 160

Arg Tyr Gly Thr Thr Val Glu Glu Glu Lys Asn His Val Leu Glu Ile
165 170 175

Ala Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Lys Glu Gln Arg Arg
180 185 190

Leu Gln Glu Gly Glu Glu Gly Ile Arg Ala Trp Thr Glu Gly Glu Lys
195 200 205

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
210 215 220

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
225 230 235 240

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
245 250

<210> 9

<211> 253

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Ten M2

<400> 9

Leu Ile Thr Gly Val Gln Gln Thr Thr Glu Arg His Asn Gln Ala Phe
1 5 10 15

Met Ala Leu Glu Gly Gln Val Ile Thr Lys Lys Leu His Ala Ser Ile
20 25 30

Arg Glu Lys Ala Gly His Trp Phe Ala Thr Thr Thr Pro Ile Ile Gly
35 40 45

Lys Gly Ile Met Phe Ala Ile Lys Glu Gly Arg Val Thr Thr Gly Val
50 55 60

Ser Ser Ile Ala Ser Glu Asp Ser Arg Lys Val Ala Ser Val Leu Asn
65 70 75 80

Asn Ala Tyr Tyr Leu Asp Lys Met His Tyr Ser Ile Glu Gly Lys Asp
85 90 95

Thr His Tyr Phe Val Lys Ile Gly Ser Ala Asp Gly Asp Leu Val Thr
100 105 110

Leu Gly Thr Thr Ile Gly Arg Lys Val Leu Glu Ser Gly Val Asn Val
115 120 125

Thr Val Ser Gln Pro Thr Leu Leu Val Asn Gly Arg Thr Arg Arg Phe
130 135 140

Thr Asn Ile Glu Phe Gln Tyr Ser Thr Leu Leu Leu Ser Ile Arg Tyr
145 150 155 160

Gly Leu Thr Pro Asp Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Asp
165 170 175

Gln Ala Arg Gln Arg Ala Leu Gly Thr Ala Trp Ala Lys Glu Gln Gln
180 185 190

Lys Ala Arg Asp Gly Arg Glu Gly Ser Arg Leu Trp Thr Glu Gly Glu
195 200 205

Lys Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr

210	215	220
Tyr Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser		
225	230	235 240
Asn Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg		
	245	250
<210> 10		
<211> 251		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> Human Ten M3		
<400> 10		
Pro Ile Phe Gly Val Gln Gln Gln Val Ala Arg Gln Ala Lys Ala Phe		
1	5	10 15
Leu Ser Leu Gly Lys Met Ala Glu Val Gln Val Ser Arg Arg Arg Ala		
	20	25 30
Gly Gly Ala Gln Ser Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile		
	35	40 45
Gly Lys Gly Val Met Leu Ala Val Ser Gln Gly Arg Val Gln Thr Asn		
	50	55 60
Val Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu		
65	70	75 80
Asn Asn Ala Phe Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Lys		
	85	90 95
Asp Thr His Tyr Phe Ile Lys Thr Thr Thr Pro Glu Ser Asp Leu Gly		
	100	105 110
Thr Leu Arg Leu Thr Ser Gly Arg Lys Ala Leu Glu Asn Gly Ile Asn		
	115	120 125

Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg
130 135 140

Phe Ala Asp Val Glu Met Gln Phe Gly Ala Leu Ala Leu His Val Arg
145 150 155 160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Ile Leu Glu Gln Ala
165 170 175

Arg Gln Arg Ala Leu Ala Arg Ala Trp Ala Arg Glu Gln Gln Arg Val
180 185 190

Arg Asp Gly Glu Glu Gly Ala Arg Leu Trp Thr Glu Gly Glu Lys Arg
195 200 205

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
210 215 220

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
225 230 235 240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Arg Arg
245 250

<210> 11

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Ten M4

<400> 11

Ser Ile Leu Gly Val Gln Cys Glu Val Gln Lys Gln Leu Lys Ala Phe
1 5 10 15

Val Thr Leu Glu Arg Phe Asp Gln Leu Tyr Gly Ser Thr Ile Thr Ser
20 25 30

Cys Leu Gln Ala Pro Lys Thr Lys Lys Phe Ala Ser Ser Gly Ser Val
35 40 45

Phe Gly Lys Gly Val Lys Phe Ala Leu Lys Asp Gly Arg Val Thr Thr
50 55 60

Asp Ile Ile Ser Val Ala Asn Glu Asp Gly Arg Arg Val Ala Ala Ile
65 70 75 80

Leu Asn His Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Asp Gly
85 90 95

Val Asp Thr His Tyr Phe Val Lys Pro Gly Pro Ser Glu Gly Asp Leu
100 105 110

Ala Ile Leu Gly Leu Ser Gly Gly Arg Arg Thr Leu Glu Asn Gly Val
115 120 125

Asn Val Thr Val Ser Gln Ile Asn Thr Val Leu Ser Gly Arg Thr Arg
130 135 140

Arg Tyr Thr Asp Ile Gln Leu Gln Tyr Gly Ala Leu Cys Leu Asn Thr
145 150 155 160

Arg Tyr Gly Thr Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Leu
165 170 175

Ala Arg Gln Arg Ala Val Arg Gln Ala Trp Ala Arg Glu Gln Gln Arg
180 185 190

Leu Arg Glu Gly Glu Glu Gly Leu Arg Ala Trp Thr Glu Gly Glu Lys
195 200 205

Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
210 215 220

Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
225 230 235 240

Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
245 250

<210> 12

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish Ten M3

<400> 12

Ser Ile Ser Gly Val Gln Gln Glu Val Met Arg Gln Ala Lys Ala Phe
1 5 10 15

Leu Ser Phe Glu Arg Met Pro Glu Ile Gln Leu Ser Arg Arg Arg Ser
20 25 30

Ser Arg Glu Lys Pro Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile
35 40 45

Gly Lys Gly Val Met Leu Ala Ile Thr Ser Lys Gly Gln Val Ala Thr
50 55 60

Asn Ala Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Val Thr Val
65 70 75 80

Leu Asn Asn Ala Phe Tyr Leu Glu Asp Leu His Phe Thr Val Glu Gly
85 90 95

Arg Asp Thr His Tyr Phe Ile Lys Thr Ser Leu Pro Glu Ser Asp Leu
100 105 110

Gly Ala Leu Arg Leu Thr Ser Gly Arg Lys Ser Leu Glu Asn Gly Val
115 120 125

Asn Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg
130 135 140

Arg Phe Ala Asp Val Glu Leu Gln Tyr Gly Ala Leu Ala Leu His Val
145 150 155 160

Arg Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Gln
165 170 175

Ala Arg Gln Arg Ala Leu Ser Ser Ala Trp Ala Arg Glu Gln Gln Arg
180 185 190

Val Arg Asp Gly Glu Glu Gly Val Arg Leu Trp Thr Glu Gly Glu Lys

195		200		205
Arg Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr				
210		215		220
Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn				
225		230		235 240
Val Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg				
	245		250	

<210> 13

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Rainbow Trout TCAP3 (40a.a.)

<400> 13

Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val
1 5 10 15
Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
20 25 30
Gln Phe Leu Arg Gln Ser Glu Ile
35 40

<210> 14

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Rainbow Trout TCAP 3 (41a.a.)

<400> 14

Arg Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr
1 5 10 15

Val Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
20 25 30

Ile Gln Phe Leu Arg Gln Ser Glu Ile
35 40

<210> 15

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Rainbow Trout preTCAP3 (43 a.a.)

<400> 15

Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val
1 5 10 15

Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
35 40

<210> 16

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Rainbow Trout preTCAP3 (44 a.a.)

<400> 16

Arg Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr
1 5 10 15

Val Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
20 25 30

Ile Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
35 40

<210> 17

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Rainbow Trout TCAP3 (120 n.a.)

<400> 17
cagctgctga gcgggaggaa gggtctgggc tacgacgggt actacgtcct ctccatagag 60
cagtaccccg agctagcaga ctccgctaac aacatccagt tcctcaggca gagcgaaata 120

<210> 18

<211> 123

<212> DNA

<213> Artificial Sequence

<220>

<223> Rainbow Trout TCAP3 (123 n.a.)

<400> 18
aggcagctgc tgagcgggag gaagggttctg ggctacgacg ggtactacgt cctctccata 60
gagcagtacc ccgagctagc agactccgct aacaacatcc agttcctcag gcagagcgaa 120
ata 123

<210> 19

<211> 129

<212> DNA

<213> Artificial Sequence

<220>

<223> Rainbow Trout preTCAP3 (129 n.a.)

<400> 19

cagctgctga gcgaggaggaa ggttctgggc tacgacgggt actacgtcct ctccatagag	60
cagtaccccg agctagcaga ctccgctaac aacatccagt tcctcaggca gagcgaaata	120
gggaagagg	129

<210> 20

<211> 132

<212> DNA

<213> Artificial Sequence

<220>

<223> Rainbow Trout preTCAP3 (132 n.a.)

<400> 20

aggcagctgc tgagcgggag gaaggttctg ggctacgacg ggtactacgt cctctccata	60
gagcagtacc ccgagctagc agactccgct aacaacatcc agttcctcag gcagagcgaa	120
ataggaaga gg	132

<210> 21

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP3 (40 a.a.)

<400> 21

Gln	Leu	Leu	Ser	Ser	Gly	Lys	Val	Leu	Gly	Tyr	Asp	Gly	Tyr	Tyr	Val
1				5					10					15	

Leu	Ser	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ala	Asn	Asn	Val
			20					25					30		

Gln Phe Leu Arg Gln Ser Glu Ile
35 40

<210> 22

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP3 (41 a.a.)

<400> 22

Arg Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
20 25 30

Val Gln Phe Leu Arg Gln Ser Glu Ile
35 40

<210> 23

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish preTCAP3 (43 a.a.)

<400> 23

Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val
1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Val
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
35 40

<210> 24

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish preTCAP3 (44 a.a.)

<400> 24

Arg	Gln	Leu	Leu	Ser	Ser	Gly	Lys	Val	Leu	Gly	Tyr	Asp	Gly	Tyr	Tyr
1				5					10					15	

Val	Leu	Ser	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ala	Asn	Asn
			20					25					30		

Val	Gln	Phe	Leu	Arg	Gln	Ser	Glu	Ile	Gly	Lys	Arg
		35					40				

<210> 25

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP3 (120 n.a.)

<400> 25

cagttgctca	gctctgggaa	ggtgctgggt	tacgatgggt	actatgtact	atcagtggag	60
caataccctg	aactggccga	cagtgccaac	aatgtccagt	tcttgaggca	gagtgagata	120

<210> 26

<211> 123

<212> DNA

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP3 (123 n.a.)

<400> 26

aggcagttgc tcagctctgg gaaggtgctg ggttacgatg gttactatgt actatcagtg 60

gagcaatacc ctgaactggc cgacagtgcc aacaatgtcc agttcttgag gcagagtgag 120

ata 123

<210> 27

<211> 129

<212> DNA

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP3 (129 n.a.)

<400> 27

cagttgctca gctctgggaa ggtgctgggt tacgatgggt actatgtact atcagtggag 60

caataccctg aactggccga cagtgccaac aatgtccagt tcttgaggca gagtgagata 120

gggaagagg 129

<210> 28

<211> 132

<212> DNA

<213> Artificial Sequence

<220>

<223> Zebrafish preTCAP3 (132 n.a.)

<400> 28

aggcagttgc tcagctctgg gaaggtgctg ggttacgatg gttactatgt actatcagtg 60

gagcaatacc ctgaactggc cgacagtgcc aacaatgtcc agttcttgag gcagagtgag 120

atagggaaga gg 132

<210> 29

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP4 (40 a.a.)

<400> 29

Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr Ile
1 5 10 15

Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn Val
20 25 30

His Phe Trp Arg Gln Thr Glu Met
35 40

<210> 30

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP4 (41 a.a.)

<400> 30

Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr
1 5 10 15

Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn
20 25 30

Val His Phe Trp Arg Gln Thr Glu Met
35 40

<210> 31

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish preTCAP4 (43 a.a.)

<400> 31

Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr Ile
1 5 10 15

Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn Val
20 25 30

His Phe Trp Arg Gln Thr Glu Met Gly Arg Arg
35 40

<210> 32

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish preTCAP4 (44 a.a.)

<400> 32

Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr
1 5 10 15

Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn
20 25 30

Val His Phe Trp Arg Gln Thr Glu Met Gly Arg Arg
35 40

<210> 33

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP4 (120 n.a.)

<400> 33

cagctcctaa gctctggacg tgtacagggc tacgaaggct tctacatagt atcagtcgac 60

cagttcccag agttgactga caacataaat aacgtccatt tctggcgaca gactgagatg 120

<210> 34

<211> 123

<212> DNA

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP4 (123 n.a.)

<400> 34

cagcagctcc taagctctgg acgtgtacag ggctacgaag gcttctacat agtatcagtc 60

gaccagttcc cagagttgac tgacaacata aataacgtcc atttctggcg acagactgag 120

atg 123

<210> 35

<211> 129

<212> DNA

<213> Artificial Sequence

<220>

<223> Zebrafish preTCAP4 (129 n.a.)

<400> 35

cagctcctaa gctctggacg tgtacagggc tacgaaggct tctacatagt atcagtcgac 60

cagttcccag agttgactga caacataaat aacgtccatt tctggcgaca gactgagatg 120

ggacgcagg 129

<210> 36

<211> 132

<212> DNA

<213> Artificial Sequence

<220>

<223> Zebrafish preTCAP4 (132 n.a.)

<400> 36

cagcagctcc taagctctgg acgtgtacag ggctacgaag gcttctacat agtatcagtc 60

gaccagttcc cagagttgac tgacaacata aataacgtcc atttctggcg acagactgag 120

atggggacgca gg 132

<210> 37

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse TCAP1 (40 a.a.)

<400> 37

Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
1 5 10 15

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
20 25 30

His Phe Met Arg Gln Ser Glu Ile
35 40

<210> 38

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse TCAP1 (41 a.a.)

<400> 38

Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
20 25 30

Ile His Phe Met Arg Gln Ser Glu Ile
35 40

<210> 39

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse preTCAP1 (43 a.a.)

<400> 39

Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
1 5 10 15

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
20 25 30

His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
35 40

<210> 40

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse preTCAP1 (44 a.a.)

<400> 40

Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
20 25 30

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
35 40

<210> 41

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse TCAP1 (120 n.a.)

<400> 41
cagcttttgg gcaccgggag ggtgcagggg tatgatgggt attttgtctt gtctgttgag 60
cagtatttag aactttcaga cagtgcacaac aatattcact tcatgagaca gagtgaaata 120

<210> 42

<211> 123

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse TCAP1 (123 n.a.)

<400> 42
cagcagcttt tgggcaccgg gaggggtgcag gggatatgatg ggtattttgt cttgtctggt 60
gagcagtatt tagaactttc agacagtgcc aacaatattc acttcatgag acagagtgaa 120
ata 123

<210> 43

<211> 129

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse preTCAP1 (129 n.a.)

<400> 43

cagcttttgg gcaccgggag ggtgcagggg tatgatgggt attttgtctt gtctgttgag 60

cagtatttag aactttcaga cagtgccaac aatattcact tcatgagaca gagtgaaata 120

ggcaggagg 129

<210> 44

<211> 132

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse preTCAP1 (132 n.a.)

<400> 44

cagcagcttt tgggcaccgg gaggggtgcag gggtatgatg ggtattttgt cttgtctggt 60

gagcagtatt tagaactttc agacagtgcc aacaatattc acttcatgag acagagtgaa 120

ataggcagga gg 132

<210> 45

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse TCAP2 (40 a.a.)

<400> 45

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
1 5 10 15

Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
20 25 30

Gln Phe Leu Arg Gln Asn Glu Ile
35 40

<210> 46

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse TCAP2 (41 a.a.)

<400> 46

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
1 5 10 15

Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn
20 25 30

Ile Gln Phe Leu Arg Gln Asn Glu Met
35 40

<210> 47

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse preTCAP2 (43 a.a)

<400> 47

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
1 5 10 15

Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
20 25 30

Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
35 40

<210> 48

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse preTCAP2 (44 a.a.)

<400> 48

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
1 5 10 15

Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn
20 25 30

Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
35 40

<210> 49

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse TCAP2 (120 n.a.)

<400> 49

caactcctga gcacgggacg ggtacaaggt tatgagggct attacgtact tccgggtgaa 60

cagtaccccg agctggcaga cagtagcagc aacatccagt tcttaagaca gaatgagagg 120

<210> 50

<211> 123

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse TCAP 2 (123 n.a.)

<400> 50

cagcaactcc tgagcacggg acgggtacaa ggttatgagg gctattacgt acttccggtg 60

gaacagtacc cggagctggc agacagtagc agcaacatcc agttcttaag acagaatgag 120

atg 123

<210> 51

<211> 129

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse preTCAP2 (129 n.a.)

<400> 51

caactcctga gcacgggacg ggtacaaggt tatgagggct attacgtact tccggtggaa 60

cagtacccgg agctggcaga cagtagcagc aacatccagt tcttaagaca gaatgagatg 120

ggaaagagg 129

<210> 52

<211> 132

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse preTCAP2 (132 n.a.)

<400> 52

cagcaactcc tgagcacggg acgggtacaa ggttatgagg gctattacgt acttccggtg 60

gaacagtacc cggagctggc agacagtagc agcaacatcc agttcttaag acagaatgag 120

atgggaaaga gg 132

<210> 53

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse TCAP3 (40 a.a.)

<400> 53

Gln	Leu	Leu	Ser	Ala	Gly	Lys	Val	Gln	Gly	Tyr	Asp	Gly	Tyr	Tyr	Val
1				5					10					15	

Leu	Ser	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ala	Asn	Asn	Ile
			20					25					30		

Gln	Phe	Leu	Arg	Gln	Ser	Glu	Ile
		35					40

<210> 54

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse TCAP3 (41 a..a)

<400> 54

Arg	Gln	Leu	Leu	Ser	Ala	Gly	Lys	Val	Gln	Gly	Tyr	Asp	Gly	Tyr	Tyr
1				5					10					15	

Val	Leu	Ser	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ala	Asn	Asn
			20					25					30		

Ile	Gln	Phe	Leu	Arg	Gln	Ser	Glu	Ile
		35						40

<210> 55

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse preTCAP3 (43 a.a.)

<400> 55

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
35 40

<210> 56

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse preTCAP3 (44 a.a.)

<400> 56

Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
20 25 30

Ile Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
35 40

<210> 57

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse TCAP3 (120 n.a.)

<400> 57

cagctgctga gcgctggcaa ggtgcagggc tacgatgggt actacgtact gtcgggtggag 60

cagtaccccg agctggctga cagtgccaac aacatccagt tcttgcgaca aagtgagatc 120

<210> 58

<211> 123

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse TCAP3 (123 n.a.)

<400> 58

cggcagctgc tgagcgctgg caaggtgcag ggctacgatg ggtactacgt actgtcgggtg 60

gagcagtacc ccgagctggc tgacagtgcc aacaacatcc agttcttgcg acaaagtgag 120

atc 123

<210> 59

<211> 129

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse preTCAP3 (129 n.a.)

<400> 59

cagctgctga gcgctggcaa ggtgcagggc tacgatgggt actacgtact gtcgggtggag 60

cagtaccccg agctggctga cagtgccaac aacatccagt tcttgcgaca aagtgagatc 120

ggcaagagg 129

<210> 60

<211> 132

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse preTCAP3 (132 n.a.)

<400> 60

cggcagctgc tgagcgctgg caaggtgcag ggctacgatg ggtactacgt actgtcgggtg 60

gagcagtacc ccgagctggc tgacagtgcc aacaacatcc agttcttgcg acaaagtgag 120

atcggcaaga gg 132

<210> 61

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse TCAP4 (40 a.a.)

<400> 61

Gln	Val	Leu	Asn	Thr	Gly	Arg	Val	Gln	Gly	Tyr	Asp	Gly	Phe	Phe	Val
1				5				10					15		

Thr	Ser	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ser	Asp	Ser	Ala	Asn	Asn	Ile
			20					25					30		

His	Phe	Met	Arg	Gln	Ser	Glu	Met
		35				40	

<210> 62

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse TCAP4 (41 a.a.)

<400> 62

Gln Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
1 5 10 15

Val Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
20 25 30

Ile His Phe Met Arg Gln Ser Glu Met
35 40

<210> 63

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse preTCAP4 (43 a.a.)

<400> 63

Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val
1 5 10 15

Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile
20 25 30

His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
35 40

<210> 64

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse preTCAP4 (44 a.a.)

<400> 64

Gln	Gln	Val	Leu	Asn	Thr	Gly	Arg	Val	Gln	Gly	Tyr	Asp	Gly	Phe	Phe
1				5					10					15	

Val	Thr	Ser	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ser	Asp	Ser	Ala	Asn	Asn
			20					25					30		

Ile	His	Phe	Met	Arg	Gln	Ser	Glu	Met	Gly	Arg	Arg
		35					40				

<210> 65

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse TCAP4 (120 n.a.)

<400> 65	
cagggtgctga acacggggcg ggtgcaaggc tacgacggct tctttgtgac ctcggtcgag	60
cagtacccag aactgtcaga cagcgccaac aatatccact tcatgagaca gagcgagatg	120

<210> 66

<211> 123

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse TCAP4 (123 n.a.)

<400> 66	
cagcaggtgc tgaacacggg gcgggtgcaa ggctacgacg gcttctttgt gacctcggtc	60
gagcagtacc cagaactgtc agacagcgcc aacaatatcc acttcatgag acagagcgag	120
atg	123

<210> 67

<211> 129

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse preTCAP4 (129 n.a.)

<400> 67

caggtgctga acacggggcg ggtgcaaggc tacgacggct tctttgtgac ctcggtcgag 60

cagtaccag aactgtcaga cagcgccaac aatatccact tcatgagaca gagcgagatg 120

ggccgaagg 129

<210> 68

<211> 132

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse preTCAP4 (132 n.a.)

<400> 68

cagcaggtgc tgaacacggg gcgggtgcaa ggctacgacg gcttctttgt gacctcggtc 60

gagcagtacc cagaactgtc agacagcgcc aacaatatcc acttcatgag acagagcgag 120

atgggccgaa gg 132

<210> 69

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TCAP1 (40 a.a.)

<400> 69

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
1 5 10 15

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
20 25 30

His Phe Met Arg Gln Ser Glu Ile
35 40

<210> 70

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TCAP1 (41 a.a.)

<400> 70

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
20 25 30

Ile His Phe Met Arg Gln Ser Glu Ile
35 40

<210> 71

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Human preTCAP1 (43 a.a.)

<400> 71

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
1 5 10 15

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
20 25 30

His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
35 40

<210> 72

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Human preTCAP1 (44 a.a.)

<400> 72

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
20 25 30

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
35 40

<210> 73

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Human TCAP1 (120 n.a.)

<400> 73

cagcttttga gcactgggcg ggtacaaggt tacgatgggt attttgtttt gtctgttgag 60

cagtatttag aactttctga cagtgcgaat aatattcact ttatgagaca gagcgaaata 120

<210> 74

<211> 123

<212> DNA

<213> Artificial Sequence

<220>

<223> Human TCAP1 (123 n.a.)

<400> 74

cagcagcttt tgagcactgg gcgggtacaa ggttacgatg ggtatattgt tttgtctggt 60

gagcagtatt tagaactttc tgacagtgcc aataatattc actttatgag acagagcgaa 120

ata 123

<210> 75

<211> 129

<212> DNA

<213> Artificial Sequence

<220>

<223> Human preTCAP1 (129 n.a.)

<400> 75

cagcttttga gcaactgggcg ggtacaaggt tacgatgggt attttgtttt gtctgttgag 60

cagtatttag aactttctga cagtgcgaat aatattcact ttatgagaca gagcgaaata 120

ggcaggagg 129

<210> 76

<211> 132

<212> DNA

<213> Artificial Sequence

<220>

<223> Human preTCAP1 (132 n.a.)

<400> 76

cagcagcttt tgagcactgg gcgggtacaa ggttacgatg ggtatattgt tttgtctggt 60

gagcagtatt tagaactttc tgacagtgcc aataatattc actttatgag acagagcgaa 120

ataggcagga gg 132

<210> 77

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TCAP2 (40 a.a.)

<400> 77

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
1 5 10 15

Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
20 25 30

Gln Phe Leu Arg Gln Asn Glu Met
35 40

<210> 78

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Human preTCAP2 (41 a.a.)

<400> 78

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
1 5 10 15

Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn
20 25 30

Ile Gln Phe Leu Arg Gln Asn Glu Met

35

40

<210> 79

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Human preTCAP2 (43 a.a.)

<400> 79

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
1 5 10 15

Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
20 25 30

Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
35 40

<210> 80

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Human preTCAP2 (44 a.a.)

<400> 80

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
1 5 10 15

Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn
20 25 30

Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
35 40

<210> 81

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Human TCAP2 (120 n.a.)

<400> 81

cagcttctga gcaccgggcg cgtgcaaggg tacgagggat attacgtgct tcccgtggag 60

caatacccag agcttgcaga cagtagcagc aacatccagt ttttaagaca gaatgagatg 120

<210> 82

<211> 123

<212> DNA

<213> Artificial Sequence

<220>

<223> Human TCAP2 (123 n.a.)

<400> 82

cagcagcttc tgagcaccgg gcgcgtgcaa gggtagcagg gatattacgt gcttcccgtg 60

gagcaatacc cagagcttgc agacagtagc agcaacatcc agtttttaag acagaatgag 120

atg 123

<210> 83

<211> 129

<212> DNA

<213> Artificial Sequence

<220>

<223> Human preTCAP2 (129 n.a.)

<400> 83

cagcttctga gcaccgggcg cgtgcaaggg tacgagggat attacgtgct tcccgtggag 60

caataccag agcttgcaga cagtagcagc aacatccagt ttttaagaca gaatgagatg 120
ggaaagagg 129

<210> 84

<211> 132

<212> DNA

<213> Artificial Sequence

<220>

<223> Human preTCAP2 (132 n.a.)

<400> 84
cagcagcttc tgagcaccgg gcgcgtgcaa gggtagcagg gatattacgt gcttcccggtg 60
gagcaatacc cagagcttgc agacagtagc agcaacatcc agtttttaag acagaatgag 120
atgggaaaga gg 132

<210> 85

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TCAP3 (40 a.a.)

<400> 85

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile
35 40

<210> 86

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TCAP3 (41 a.a.)

<400> 86

Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
20 25 30

Ile Gln Phe Leu Arg Gln Ser Glu Ile
35 40

<210> 87

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Human preTCAP3 (43 a.a.)

<400> 87

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile Gly Arg Arg
35 40

<210> 88

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Human preTCAP3 (44 a.a.)

<400> 88

Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
20 25 30

Ile Gln Phe Leu Arg Gln Ser Glu Ile Gly Arg Arg
35 40

<210> 89

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Human TCAP3 (120 n.a.)

<400> 89

cagctgctga ggcgcggcaa ggtgcagggc tacgacgggt actacgtact ctcggtggag 60

cagtaccccg agctggccga cagcgccaac aacatccagt tcctgcggca gagcgagatc 120

<210> 90

<211> 123

<212> DNA

<213> Artificial Sequence

<220>

<223> Human TCAP3 (123 n.a.)

<400> 90

cggcagctgc tgagcgccgg caaggtgcag ggctacgacg ggtactacgt actctcgggtg 60

gagcagtacc ccgagctggc cgacagcgcc aacaacatcc agttcctgcg gcagagcgag 120

atc 123

<210> 91

<211> 129

<212> DNA

<213> Artificial Sequence

<220>

<223> Human preTCAP (129 n.a.)

<400> 91
cagctgctga gcgccggcaa ggtgcagggc tacgacgggt actacgtact ctcggtggag 60
cagtaccccg agctggccga cagcgccaac aacatccagt tcctgcggca gagcgagatc 120
ggcaggagg 129

<210> 92

<211> 132

<212> DNA

<213> Artificial Sequence

<220>

<223> Human preTCAP3 (132 n.a.)

<400> 92
cggcagctgc tgagcgccgg caaggtgcag ggctacgacg ggtactacgt actctcggtg 60
gagcagtacc ccgagctggc cgacagcgcc aacaacatcc agttcctgcg gcagagcgag 120
atcggcagga gg 132

<210> 93

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TCAP4 (40 a.a.)

<400> 93

Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val
1 5 10 15

Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile
20 25 30

His Phe Met Arg Gln Ser Glu Met
35 40

<210> 94

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Human TCAP4 (41 a.a.)

<400> 94

Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
1 5 10 15

Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
20 25 30

Ile His Phe Met Arg Gln Ser Glu Met
35 40

<210> 95

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Human preTCAP4 (43 a..a)

<400> 95

Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val
1 5 10 15

Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile
20 25 30

His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
35 40

<210> 96

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Human preTCAP4 (44 a.a.)

<400> 96

Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
1 5 10 15

Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
20 25 30

Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
35 40

<210> 97

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Human TCAP4 (120 n.a.)

<400> 97

cagggtgctga gcacagggcg ggtgcaaggc tacgacggct ttttcgtgat ctctgtcgag

60

cagtaccag aactgtcaga cagcgccaac aacatccact tcatgagaca gagcgagatg 120

<210> 98

<211> 123

<212> DNA

<213> Artificial Sequence

<220>

<223> Human TCAP4 (123 n.a.)

<400> 98

cagcaggtgc tgagcacagg gcgggtgcaa ggctacgacg gctttttcgt gatctctgtc 60

gagcagtacc cagaactgtc agacagcgcc aacaacatcc acttcatgag acagagcgag 120

atg 123

<210> 99

<211> 129

<212> DNA

<213> Artificial Sequence

<220>

<223> Human preTCAP4 (129 n.a.)

<400> 99

caggtgctga gcacagggcg ggtgcaaggc tacgacggct ttttcgtgat ctctgtcgag 60

cagtaccag aactgtcaga cagcgccaac aacatccact tcatgagaca gagcgagatg 120

ggccggagg 129

<210> 100

<211> 132

<212> DNA

<213> Artificial Sequence

<220>

<223> Human preTCAP4 (132 n.a.)

<400> 100

cagcaggtgc tgagcacagg gcgggtgcaa ggctacgacg gctttttcgt gatctctgtc 60

gagcagtacc cagaactgtc agacagcgcc aacaacatcc acttcatgag acagagcgag 120

atgggccgga gg 132

<210> 101

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> G. gallus TCAP-1

<400> 101

Gln Gln Leu Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
20 25 30

Ile His Phe Met Arg Gln Ser Glu Ile
35 40

<210> 102

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP-4

<400> 102

Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr
1 5 10 15

Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn

20 25 30

Val His Phe Trp Arg Gln Thr Glu Met
35 40

<210> 103

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> D. melanogaster Ten-m gene product

<400> 103

Glu Leu Val Gln His Gly Asp Val Asp Gly Trp Asn Gly Asp Ile His
1 5 10 15

Ser Ile His Lys Tyr Pro Gln Leu Ala Asp Pro Gly Asn Val Ala Phe
20 25 30

Gln Arg Asp Ala Lys
35

<210> 104

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Human CRF TCAP like region

<400> 104

Ser Glu Glu Pro Pro Ile Ser Leu Asp Leu Thr Phe His Leu Leu Arg
1 5 10 15

Glu Val Leu Glu Met Ala Arg Ala Glu Gln Leu Ala Gln Gln Ala His
20 25 30

Ser Asn Arg Lys Leu Met Glu Ile Ile
35 40

<210> 105

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Human urocortin TCAP-like region

<400> 105

Asp Asn Pro Ser Leu Ser Ile Asp Leu Thr Phe His Leu Leu Arg Thr
1 5 10 15

Leu Leu Glu Leu Ala Arg Thr Gln Ser Gln Arg Glu Arg Ala Glu Gln
20 25 30

Asn Arg Ile Ile Phe Asp Ser Val
35 40

<210> 106

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Human urocortin 2 TCAP-like region

<400> 106

Ile Val Leu Ser Leu Asp Val Pro Ile Gly Leu Leu Gln Ile Leu Leu
1 5 10 15

Glu Gln Ala Arg Ala Arg Ala Ala Arg Glu Gln Ala Thr Thr Asn Ala
20 25 30

Arg Ile Leu Ala Arg Val
35

<210> 107

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Human urocortin 3 TCAP=like region

<400> 107

Phe	Thr	Leu	Ser	Leu	Asp	Val	Pro	Thr	Asn	Ile	Met	Asn	Leu	Leu	Phe
1				5					10					15	

Asn	Ile	Ala	Lys	Ala	Lys	Asn	Leu	Arg	Ala	Gln	Ala	Ala	Ala	Asn	Ala
			20					25					30		

His	Leu	Met	Ala	Gln	Ile
		35			

<210> 108

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> L. migratoria DP

<400> 108

Met	Gly	Met	Gly	Pro	Ser	Leu	Ser	Ile	Val	Asn	Pro	Met	Asp	Val	Leu
1				5					10					15	

Arg	Gln	Arg	Leu	Leu	Leu	Glu	Ile	Ala	Arg	Arg	Arg	Leu	Arg	Asp	Ala
			20					25					30		

Glu	Glu	Gln	Ile	Lys	Ala	Asn	Lys	Asp	Phe	Leu	Gln	Gln	Ile
		35					40					45	

<210> 109

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> A. domesticus DP

<400> 109

Thr Gly Ala Gln Ser Leu Ser Ile Val Ala Pro Leu Asp Val Leu Arg
1 5 10 15

Gln Arg Leu Met Asn Glu Leu Asn Arg Arg Arg Met Arg Glu Leu Gln
20 25 30

Gly Ser Arg Ile Gln Gln Asn Arg Gln Leu Leu Thr Ser Ile
35 40 45

<210> 110

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> T. molitor DP

<400> 110

Ser Pro Thr Ile Ser Ile Thr Ala Pro Ile Asp Val Leu Arg Lys Thr
1 5 10 15

Trp Glu Gln Glu Arg Ala Arg Lys Gln Met Val Ala Gln Asn Asn Arg
20 25 30

Glu Phe Leu Asn Ser Leu Asn
35

<210> 111

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> M. sexta DP-1

<400> 111

Arg	Met	Pro	Ser	Leu	Ser	Ile	Asp	Leu	Pro	Met	Ser	Val	Leu	Arg	Gln
1				5				10					15		

Lys	Leu	Ser	Leu	Glu	Lys	Glu	Arg	Lys	Val	His	Ala	Leu	Arg	Ala	Ala
			20					25					30		

Ala	Asn	Arg	Asn	Phe	Leu	Asn	Asp	Ile
		35					40	

<210> 112

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> M. sexta DP-II

<400> 112

Ser	Leu	Ser	Val	Asn	Pro	Ala	Val	Asp	Ile	Leu	Gln	His	Arg	Tyr	Met
1				5				10					15		

Glu	Lys	Val	Ala	Gln	Asn	Asn	Arg	Asn	Phe	Leu	Asn	Arg	Val
			20					25				30	

<210> 113

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> P. Americana

<400> 113

Thr Gly Ser Gly Pro Ser Leu Ser Ile Val Asn Pro Leu Asp Val Leu
1 5 10 15

Arg Gln Arg Leu Leu Leu Glu Ile Ala Arg Arg Arg Met Arg Gln Ser
20 25 30

Gln Asp Gln Ile Gln Asn Arg Glu Ile Leu Gln Thr Ile
35 40 45

<210> 114

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> O. keta CRP

<400> 114

Ser Asp Asp Pro Pro Ile Ser Leu Asp Leu Thr Phe His Met Leu Arg
1 5 10 15

Gln Met Asn Glu Met Ser Arg Ala Glu Gln Leu Gln Gln Gln Ala His
20 25 30

Ser Asn Arg Lys Met Met Glu Ile Phe
35 40

<210> 115

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> R. norvegicus

<400> 115

Asp Asp Pro Pro Leu Ser Ile Asp Leu Thr Phe His Leu Leu Arg Thr
1 5 10 15

Leu Leu Glu Leu Ala Arg Thr Gln Ser Gln Arg Glu Arg Ala Glu Gln
20 25 30

Asn Arg Ile Ile Phe Asp Ser Val
35 40

<210> 116

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> *P. sauvageii*

<400> 116

Gln Gly Pro Pro Ile Ser Ile Asp Leu Ser Leu Glu Leu Leu Arg Lys
1 5 10 15

Met Ile Glu Ile Glu Lys Gln Glu Lys Glu Lys Gln Gln Ala Ala Asn
20 25 30

Asn Arg Leu Leu Leu
35

<210> 117

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> *C. carpio* US

<400> 117

Asn Asp Asp Pro Pro Ile Ser Ile Asp Leu Thr Phe His Leu Leu Arg
1 5 10 15

Asn Met Ile Glu Met Ala Arg Asn Glu Asn Gln Arg Glu Gln Ala Gly
20 25 30

Leu Asn Arg Lys Tyr Leu Asp Glu Val
35 40

<210> 118

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> M. Musculus UCN2

<400> 118

Val Ile Leu Ser Leu Asp Val Pro Ile Gly Leu Leu Arg Ile Leu Leu
1 5 10 15

Glu Gln Ala Arg Tyr Lys Ala Ala Arg Asn Gln Ala Ala Thr Asn Ala
20 25 30

Gln Ile Leu Ala His Val
35

<210> 119

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> R. dano UCN2

<400> 119

Leu Thr Leu Ser Leu Asp Val Pro Thr Asn Ile Met Asn Val Leu Phe
1 5 10 15

Asp Val Ala Lys Ala Lys Asn Leu Arg Ala Lys Ala Ala Glu Asn Ala

20

25

30

Arg Leu Leu Ala His Ile
35

<210> 120

<211> 305

<212> DNA

<213> Artificial Sequence

<220>

<223> Hamster 305bp urocortin cDNA probe examples "cloning mRNA"

<400> 120
attcaccgcc gctcgggata tgagcctgca ggcgagcggc agcgacggga agaccttccg 60
ctgtccatcg acctcacatt ccacctgcta cggaccctgc tggagatggc ccggacacag 120
agccaacgcg agcgagcaga gcagaaccga atcataactca acgcggtggg caagtgatcg 180
gcccgggtgtg ggacccccaaa aggctcgacc ctttccccta cctaccccgg ggctgaagtc 240
acgcgaccga agtcggctta gtcccgcggt gcagcgccctc ccagagttac cctgaacaat 300
cccgc 305

<210> 121

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> TCAP1 fwd primer

<400> 121
acgtcagtgt tgatgggagg acta 24

<210> 122

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> TCAP1 rvs primer

<400> 122

cctcctgcct atttcactct gtctcat

27

<210> 123

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> TCAP2 Fwd primer

<400> 123

tcgagggcaa ggacacacac tactt

25

<210> 124

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> TCAP2 rvs primer

<400> 124

aagaactgga tggtgctgct actgtc

26

<210> 125

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> TCAP3 fwd primer

<400> 125

caacaacgcc ttctacctgg agaac

25

<210> 126

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> TCAP3 rvs primer

<400> 126

tggtggtggc actgtcagcc a

21

<210> 127

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> TCAP4 fwd primer

<400> 127

tttgctcca gtggttccat ctt

23

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> TCAP4 rvs primer

<400> 128

tggatattgt tggcgctgtc tgac

24

<210> 129

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conserved motif between CRF and TCAP I/L S X X (X)-L/V at amino
terminus

<220>

<221> MISC_FEATURE

<222> (1) .. (1)

<223> X=I or L

<220>

<221> MISC_FEATURE

<222> (3) .. (3)

<223> X=T or A

<220>

<221> MISC_FEATURE

<222> (4) .. (4)

<223> X=L, I or G

<220>

<221> MISC_FEATURE

<222> (5) .. (5)

<223> X=D, R or K

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> X=L or V

<400> 129

Xaa Ser Xaa Xaa Xaa Xaa
1 5

<210> 130

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Conserved motif between CRF and TCAP - In middle L/V-L/I-X-V/aliphatic residue

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> X=V or L

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> X=M, L Q, I or V

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> X=L, I or F

<220>

<221> MISC_FEATURE

<222> (3) .. (3)

<223> X=E, N, S or P

<400> 130

Xaa Xaa Xaa Xaa

1

<210> 131

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Conserved motif between CRF and TCAP N/I/A-H/basic residue -I/L/F
/-aliphatic at carboxy terminus

<220>

<221> MISC_FEATURE

<222> (2) .. (2)

<223> X=R, A or I

<220>

<221> MISC_FEATURE

<222> (3) .. (3)

<223> X=H or basic residues, K, I, R or Q

<220>

<221> MISC_FEATURE

<222> (4) .. (4)

<223> X=I, L or F

<400> 131

Asn Xaa Xaa Xaa
1

<210> 132

<211> 8964

<212> DNA

<213> Mus musculus

<220>

<221> exon

<222> (50)..(8197)

<223>

<400> 132

aagttctaag aagccggacc gatgtgcaca gagaaggaat gaaggaagt atg gat gtg 58
Met Asp Val
1

aag gaa cgc agg cct tac tgc tcc ttg acc aag agc aga cgg gaa aag 106
Lys Glu Arg Arg Pro Tyr Cys Ser Leu Thr Lys Ser Arg Arg Glu Lys
5 10 15

gaa agg cgc tat aca aat tcg tcc gcg gac aat gag gag tgt agg gtc 154
Glu Arg Arg Tyr Thr Asn Ser Ser Ala Asp Asn Glu Glu Cys Arg Val
20 25 30 35

ccc acg cag aag tcc tat agt tcc agt gaa acc ttg aaa gct ttc gat 202
Pro Thr Gln Lys Ser Tyr Ser Ser Ser Glu Thr Leu Lys Ala Phe Asp
40 45 50

cat gat tat tca cgg ctg ctt tat gga aac aga gta aag gat ttg gtc 250
His Asp Tyr Ser Arg Leu Leu Tyr Gly Asn Arg Val Lys Asp Leu Val
55 60 65

cac aga gaa gcc gac gag tat act aga caa gga cag aat ttt acc cta 298
His Arg Glu Ala Asp Glu Tyr Thr Arg Gln Gly Gln Asn Phe Thr Leu
70 75 80

agg cag tta gga gtg tgt gaa tcc gca act cga aga gga gtg gca ttc 346
Arg Gln Leu Gly Val Cys Glu Ser Ala Thr Arg Arg Gly Val Ala Phe
85 90 95

tgt gcg gaa atg ggg ctc cct cac aga ggt tac tcc atc agt gca ggg 394
Cys Ala Glu Met Gly Leu Pro His Arg Gly Tyr Ser Ile Ser Ala Gly

100					105					110					115	
tca	gat	gcg	gat	acg	gaa	aac	gaa	gca	gtg	atg	tcc	cct	gag	cat	gcc	442
Ser	Asp	Ala	Asp	Thr	Glu	Asn	Glu	Ala	Val	Met	Ser	Pro	Glu	His	Ala	
				120					125					130		
atg	aga	ctt	tgg	ggc	agg	ggg	gtc	aaa	tcg	ggc	cgc	agt	tcc	tgc	ctg	490
Met	Arg	Leu	Trp	Gly	Arg	Gly	Val	Lys	Ser	Gly	Arg	Ser	Ser	Cys	Leu	
			135					140					145			
tca	agc	cgg	tcc	aac	tcc	gcc	ctc	acc	ctg	aca	gac	acg	gag	cac	gag	538
Ser	Ser	Arg	Ser	Asn	Ser	Ala	Leu	Thr	Leu	Thr	Asp	Thr	Glu	His	Glu	
		150					155					160				
aac	agg	tcg	gac	agt	gag	agc	gag	caa	cct	tca	aac	aac	cca	ggg	caa	586
Asn	Arg	Ser	Asp	Ser	Glu	Ser	Glu	Gln	Pro	Ser	Asn	Asn	Pro	Gly	Gln	
	165					170					175					
ccc	acc	ctg	cag	cct	ttg	ccg	cca	tcc	cac	aag	cag	cac	ccg	gcg	cag	634
Pro	Thr	Leu	Gln	Pro	Leu	Pro	Pro	Ser	His	Lys	Gln	His	Pro	Ala	Gln	
180					185					190					195	
cat	cac	ccg	tcc	atc	act	tcc	ctc	aat	aga	aac	tcc	ctg	acc	aat	aga	682
His	His	Pro	Ser	Ile	Thr	Ser	Leu	Asn	Arg	Asn	Ser	Leu	Thr	Asn	Arg	
				200					205					210		
agg	aac	cag	agt	ccg	gcc	ccg	ccg	gct	gct	ttg	ccc	gcc	gag	ctg	caa	730
Arg	Asn	Gln	Ser	Pro	Ala	Pro	Pro	Ala	Ala	Leu	Pro	Ala	Glu	Leu	Gln	
			215					220				225				
acc	aca	ccc	gag	tcc	gtc	cag	ctg	cag	gac	agc	tgg	gtc	ctt	ggc	agt	778
Thr	Thr	Pro	Glu	Ser	Val	Gln	Leu	Gln	Asp	Ser	Trp	Val	Leu	Gly	Ser	
		230					235					240				
aat	gta	cca	ctg	gaa	agc	agg	cat	ttc	cta	ttc	aaa	aca	ggg	aca	ggg	826
Asn	Val	Pro	Leu	Glu	Ser	Arg	His	Phe	Leu	Phe	Lys	Thr	Gly	Thr	Gly	
	245					250					255					
acg	acg	cca	ctg	ttc	agt	acg	gca	acc	ccg	gga	tac	aca	atg	gca	tct	874
Thr	Thr	Pro	Leu	Phe	Ser	Thr	Ala	Thr	Pro	Gly	Tyr	Thr	Met	Ala	Ser	
260					265					270					275	
ggc	tct	gtt	tat	tct	ccg	cct	acc	cgg	cca	ctt	cct	aga	aac	acc	cta	922
Gly	Ser	Val	Tyr	Ser	Pro	Pro	Thr	Arg	Pro	Leu	Pro	Arg	Asn	Thr	Leu	
				280					285					290		
tca	aga	agt	gct	ttt	aaa	ttc	aag	aag	tct	tca	aag	tac	tgc	agc	tgg	970
Ser	Arg	Ser	Ala	Phe	Lys	Phe	Lys	Lys	Ser	Ser	Lys	Tyr	Cys	Ser	Trp	
			295					300					305			
agg	tgc	acc	gca	ctg	tgt	gct	gta	ggg	gtc	tca	gtg	ctc	ctg	gcc	att	1018
Arg	Cys	Thr	Ala	Leu	Cys	Ala	Val	Gly	Val	Ser	Val	Leu	Leu	Ala	Ile	
		310					315					320				
ctc	ctc	tcc	tat	ttt	ata	gca	atg	cat	cta	ttt	ggc	ctc	aac	tgg	cac	1066
Leu	Leu	Ser	Tyr	Phe	Ile	Ala	Met	His	Leu	Phe	Gly	Leu	Asn	Trp	His	
		325					330				335					
tta	cag	cag	acg	gaa	aat	gac	aca	ttc	gag	aat	gga	aaa	gtg	aat	tct	1114

Leu 340	Gln	Gln	Thr	Glu	Asn 345	Asp	Thr	Phe	Glu	Asn 350	Gly	Lys	Val	Asn	Ser 355	
gac Asp	acc Thr	gtg Val	cca Pro	aca Thr	aac Asn	act Thr	gta Val	tcg Ser	tta Leu	cct Pro	tct Ser	ggc Gly	gac Asp	aat Asn	gga Gly	1162
aaa Lys	tta Leu	ggt Gly	gga Gly	ttt Phe	aca Thr	cat His	gaa Glu	aat Asn	aac Asn	acc Thr	ata Ile	gat Asp	tcc Ser	gga Gly	gaa Glu	1210
ctt Leu	gat Asp	att Ile	ggc Gly	cgg Arg	aga Arg	gca Ala	att Ile	caa Gln	gag Glu	gtt Val	ccc Pro	ccc Pro	ggg Gly	atc Ile	ttc Phe	1258
tgg Trp	aga Arg	tcg Ser	cag Gln	ctc Leu	ttt Phe	att Ile	gat Asp	cag Gln	cca Pro	cag Gln	ttt Phe	ctt Leu	aag Lys	ttc Phe	aac Asn	1306
atc Ile	tct Ser	ctt Leu	cag Gln	aag Lys	gat Asp	gca Ala	ttg Leu	atc Ile	gga Gly	gtg Val	tac Tyr	ggc Gly	cgg Arg	aag Lys	ggc Gly	1354
tta Leu	ccg Pro	cct Pro	tcc Ser	cat His	act Thr	cag Gln	tac Tyr	gac Asp	ttt Phe	gtg Val	gaa Glu	cta Leu	ctg Leu	gat Asp	ggt Gly	1402
agc Ser	agg Arg	tta Leu	att Ile	gcg Ala	aga Arg	gag Glu	cag Gln	cgg Arg	aac Asn	ctg Leu	gtg Val	gag Glu	tcc Ser	gaa Glu	aga Arg	1450
gcc Ala	ggg Gly	cgg Arg	cag Gln	gcg Ala	aga Arg	tct Ser	gtc Val	agc Ser	ctg Leu	cac His	gaa Glu	gct Ala	ggc Gly	ttc Phe	atc Ile	1498
cag Gln	tac Tyr	ttg Leu	gat Asp	tct Ser	gga Gly	atc Ile	tgg Trp	cat His	ctg Leu	gct Ala	ttt Phe	tat Tyr	aac Asn	gac Asp	ggg Gly	1546
aaa Lys	aac Asn	cca Pro	gag Glu	cag Gln	gtc Val	tcc Ser	ttt Phe	aac Asn	acg Thr	atc Ile	gtt Val	ata Ile	gag Glu	tct Ser	gtg Val	1594
gtg Val	gaa Glu	tgc Cys	ccc Pro	cga Arg	aat Asn	tgc Cys	cat His	gga Gly	aat Asn	gga Gly	gag Glu	tgt Cys	gtt Val	tct Ser	gga Gly	1642
act Thr	tgc Cys	cat His	tgt Cys	ttc Phe	ccc Pro	ggg Gly	ttt Phe	cta Leu	ggt Gly	ccg Pro	gat Asp	tgt Cys	tca Ser	aga Arg	gca Ala	1690
gcc Ala	tgt Cys	ccg Pro	gtg Val	ctc Leu	tgt Cys	agt Ser	ggc Gly	aac Asn	ggg Gly	caa Gln	tac Tyr	tcc Ser	aag Lys	ggc Gly	cgc Arg	1738
tgc Cys	ctg Leu	tgc Cys	ttc Phe	agt Ser	ggc Gly	tgg Trp	aag Lys	ggc Gly	acc Thr	gag Glu	tgt Cys	gac Asp	gtg Val	ccg Pro	acg Thr	1786

acc	cag	tgc	att	gac	ccg	cag	tgc	ggg	ggt	cgt	ggg	att	tgc	atc	atg	1834
Thr	Gln	Cys	Ile	Asp	Pro	Gln	Cys	Gly	Gly	Arg	Gly	Ile	Cys	Ile	Met	
580					585					590					595	
ggc	tct	tgc	gct	tgt	aac	tcg	gga	tac	aaa	gga	gaa	aac	tgt	gag	gaa	1882
Gly	Ser	Cys	Ala	Cys	Asn	Ser	Gly	Tyr	Lys	Gly	Glu	Asn	Cys	Glu	Glu	
				600					605					610		
gcg	gac	tgt	cta	gac	cct	gga	tgt	tct	aat	cac	ggg	gtg	tgt	atc	cat	1930
Ala	Asp	Cys	Leu	Asp	Pro	Gly	Cys	Ser	Asn	His	Gly	Val	Cys	Ile	His	
			615					620					625			
ggg	gaa	tgt	cac	tgc	aat	cca	ggc	tgg	ggt	ggc	agc	aac	tgt	gaa	ata	1978
Gly	Glu	Cys	His	Cys	Asn	Pro	Gly	Trp	Gly	Gly	Ser	Asn	Cys	Glu	Ile	
		630					635					640				
ctg	aag	act	atg	tgt	gca	gac	cag	tgc	tca	ggc	cac	ggg	act	tac	ctt	2026
Leu	Lys	Thr	Met	Cys	Ala	Asp	Gln	Cys	Ser	Gly	His	Gly	Thr	Tyr	Leu	
	645					650					655					
caa	gaa	agc	ggc	tcc	tgc	act	tgc	gac	cca	aat	tgg	act	ggc	ccc	gac	2074
Gln	Glu	Ser	Gly	Ser	Cys	Thr	Cys	Asp	Pro	Asn	Trp	Thr	Gly	Pro	Asp	
660					665					670					675	
tgc	tca	aat	gaa	ata	tgt	tca	gtg	gac	tgc	ggc	tca	cac	ggc	gtc	tgc	2122
Cys	Ser	Asn	Glu	Ile	Cys	Ser	Val	Asp	Cys	Gly	Ser	His	Gly	Val	Cys	
				680					685					690		
atg	ggg	ggc	tcc	tgt	cgc	tgt	gaa	gaa	ggc	tgg	acc	ggc	ccg	gcg	tgt	2170
Met	Gly	Gly	Ser	Cys	Arg	Cys	Glu	Glu	Gly	Trp	Thr	Gly	Pro	Ala	Cys	
			695				700						705			
aat	cag	aga	gct	tgc	cac	cct	cgc	tgt	gct	gag	cac	ggg	acg	tgc	aag	2218
Asn	Gln	Arg	Ala	Cys	His	Pro	Arg	Cys	Ala	Glu	His	Gly	Thr	Cys	Lys	
		710					715					720				
gac	ggc	aag	tgc	gag	tgc	agc	caa	gga	tgg	aac	gga	gag	cac	tgc	aca	2266
Asp	Gly	Lys	Cys	Glu	Cys	Ser	Gln	Gly	Trp	Asn	Gly	Glu	His	Cys	Thr	
		725				730					735					
att	gct	cac	tat	ttg	gat	aag	ata	gtt	aaa	gag	ggt	tgc	ccc	ggc	ttg	2314
Ile	Ala	His	Tyr	Leu	Asp	Lys	Ile	Val	Lys	Glu	Gly	Cys	Pro	Gly	Leu	
740					745					750					755	
tgc	aac	agc	aat	ggg	aga	tgc	aca	ctg	gac	caa	aac	ggc	tgg	cac	tgc	2362
Cys	Asn	Ser	Asn	Gly	Arg	Cys	Thr	Leu	Asp	Gln	Asn	Gly	Trp	His	Cys	
				760					765					770		
gtt	tgc	cag	cca	ggg	tgg	aga	gga	gca	ggc	tgt	gac	gta	gcc	atg	gag	2410
Val	Cys	Gln	Pro	Gly	Trp	Arg	Gly	Ala	Gly	Cys	Asp	Val	Ala	Met	Glu	
			775					780					785			
acc	ctc	tgt	aca	gac	agc	aaa	gac	aac	gaa	gga	gac	gga	ctc	att	gac	2458
Thr	Leu	Cys	Thr	Asp	Ser	Lys	Asp	Asn	Glu	Gly	Asp	Gly	Leu	Ile	Asp	
		790					795					800				
tgc	atg	gat	cct	gat	tgc	tgc	ctc	cag	agc	tcc	tgc	caa	aac	cag	ccc	2506
Cys	Met	Asp	Pro	Asp	Cys	Cys	Leu	Gln	Ser	Ser	Cys	Gln	Asn	Gln	Pro	
	805					810					815					

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Tyr	Cys	Arg	Gly	Leu	Pro	Asp	Pro	Gln	Asp	Ile	Ile	Ser	Gln	Ser	Leu	
820					825					830					835	
cag	aca	cca	tct	cag	caa	gct	gcc	aag	tcc	ttc	tat	gac	cga	atc	agt	2602
Gln	Thr	Pro	Ser	Gln	Gln	Ala	Ala	Lys	Ser	Phe	Tyr	Asp	Arg	Ile	Ser	
				840					845						850	
ttc	ctg	att	gga	tcg	gat	agc	acc	cac	gtg	ctc	cct	gga	gaa	agt	ccg	2650
Phe	Leu	Ile	Gly	Ser	Asp	Ser	Thr	His	Val	Leu	Pro	Gly	Glu	Ser	Pro	
			855					860					865			
ttc	aat	aag	agt	ctt	gcg	tcc	gtc	atc	aga	ggc	caa	gta	cta	aca	gct	2698
Phe	Asn	Lys	Ser	Leu	Ala	Ser	Val	Ile	Arg	Gly	Gln	Val	Leu	Thr	Ala	
		870					875					880				
gat	gga	acc	cca	ctt	att	ggc	gtc	aac	gtg	tcg	ttt	tta	cac	tac	tcg	2746
Asp	Gly	Thr	Pro	Leu	Ile	Gly	Val	Asn	Val	Ser	Phe	Leu	His	Tyr	Ser	
	885					890					895					
gaa	tat	gga	tat	acc	att	acc	cgc	cag	gat	gga	atg	ttt	gac	ttg	gtg	2794
Glu	Tyr	Gly	Tyr	Thr	Ile	Thr	Arg	Gln	Asp	Gly	Met	Phe	Asp	Leu	Val	
900					905					910					915	
gca	aat	ggt	ggc	gct	tct	ctg	act	ttg	gta	ttt	gag	cgt	tcc	cca	ttc	2842
Ala	Asn	Gly	Gly	Ala	Ser	Leu	Thr	Leu	Val	Phe	Glu	Arg	Ser	Pro	Phe	
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ctc	act	cag	tac	cac	act	gtg	tgg	att	ccc	tgg	aat	gtc	ttt	tat	gtg	2890
Leu	Thr	Gln	Tyr	His	Thr	Val	Trp	Ile	Pro	Trp	Asn	Val	Phe	Tyr	Val	
			935					940					945			
atg	gat	acc	ctt	gtc	atg	aag	aaa	gag	gag	aac	gac	att	ccc	agc	tgt	2938
Met	Asp	Thr	Leu	Val	Met	Lys	Lys	Glu	Glu	Asn	Asp	Ile	Pro	Ser	Cys	
		950					955					960				
gac	ctc	agt	ggc	ttt	gtg	agg	cca	agt	ccc	atc	att	gtg	tct	tca	ccg	2986
Asp	Leu	Ser	Gly	Phe	Val	Arg	Pro	Ser	Pro	Ile	Ile	Val	Ser	Ser	Pro	
	965					970					975					
tta	tcc	acc	ttc	ttc	agg	tct	tcc	cct	gag	gac	agc	ccc	atc	atc	ccc	3034
Leu	Ser	Thr	Phe	Phe	Arg	Ser	Ser	Pro	Glu	Asp	Ser	Pro	Ile	Ile	Pro	
980					985					990					995	
gag	aca	cag	gtc	ctg	cat	gaa	gaa	acc	aca	att	cca	gga	aca	gat		3079
Glu	Thr	Gln	Val	Leu	His	Glu	Glu	Thr	Thr	Ile	Pro	Gly	Thr	Asp		
				1000					1005					1010		
ttg	aaa	ctt	tcc	tac	ctg	agt	tcc	aga	gcg	gca	ggg	tac	aag	tca		3124
Leu	Lys	Leu	Ser	Tyr	Leu	Ser	Ser	Arg	Ala	Ala	Gly	Tyr	Lys	Ser		
				1015					1020					1025		
gtt	ctt	aag	att	acc	atg	acc	cag	gcc	gtc	ata	ccg	ttt	aac	ctc		3169
Val	Leu	Lys	Ile	Thr	Met	Thr	Gln	Ala	Val	Ile	Pro	Phe	Asn	Leu		
				1030					1035					1040		
atg	aag	gtc	cat	ctg	atg	gtg	gcc	gtg	gtt	ggg	aga	ctc	ttc	cag		3214
Met	Lys	Val	His	Leu	Met	Val	Ala	Val	Val	Gly	Arg	Leu	Phe	Gln		

1045										1050					1055					
aag	tgg	ttt	cct	gcc	tcg	cca	aac	ttg	gcc	tac	acg	ttc	atc	tgg	3259					
Lys	Trp	Phe	Pro	Ala	Ser	Pro	Asn	Leu	Ala	Tyr	Thr	Phe	Ile	Trp						
1060										1065					1070					
gat	aag	acg	gac	gca	tat	aat	cag	aaa	gtc	tac	ggc	ttg	tca	gag	3304					
Asp	Lys	Thr	Asp	Ala	Tyr	Asn	Gln	Lys	Val	Tyr	Gly	Leu	Ser	Glu						
1075										1080					1085					
gca	gtt	gtg	tcc	gtc	gga	tac	gag	tac	gag	tcg	tgc	ttg	gac	ctg	3349					
Ala	Val	Val	Ser	Val	Gly	Tyr	Glu	Tyr	Glu	Ser	Cys	Leu	Asp	Leu						
1090										1095					1100					
act	ctc	tgg	gaa	aag	agg	act	gcc	gtt	ttg	caa	ggc	tat	gag	ttg	3394					
Thr	Leu	Trp	Glu	Lys	Arg	Thr	Ala	Val	Leu	Gln	Gly	Tyr	Glu	Leu						
1105										1110					1115					
gat	gct	tcg	aac	atg	ggc	ggc	tgg	acg	ttg	gac	aag	cac	cat	gta	3439					
Asp	Ala	Ser	Asn	Met	Gly	Gly	Trp	Thr	Leu	Asp	Lys	His	His	Val						
1120										1125					1130					
ctg	gac	gtt	cag	aac	ggg	ata	cta	tac	aaa	gga	aat	gga	gaa	aat	3484					
Leu	Asp	Val	Gln	Asn	Gly	Ile	Leu	Tyr	Lys	Gly	Asn	Gly	Glu	Asn						
1135										1140					1145					
cag	ttc	atc	tct	cag	cag	cct	ccg	gtg	gtc	agc	agc	atc	atg	ggg	3529					
Gln	Phe	Ile	Ser	Gln	Gln	Pro	Pro	Val	Val	Ser	Ser	Ile	Met	Gly						
1150										1155					1160					
aat	ggg	cgg	agg	cgt	agc	atc	tca	tgc	cca	agt	tgc	aat	ggg	caa	3574					
Asn	Gly	Arg	Arg	Arg	Ser	Ile	Ser	Cys	Pro	Ser	Cys	Asn	Gly	Gln						
1165										1170					1175					
gct	gac	ggg	aac	aaa	ctc	ctg	gca	ccc	gtg	gcg	ctt	gcc	tgt	ggg	3619					
Ala	Asp	Gly	Asn	Lys	Leu	Leu	Ala	Pro	Val	Ala	Leu	Ala	Cys	Gly						
1180										1185					1190					
atc	gac	ggc	agt	cta	tac	gta	ggg	gat	ttc	aat	tac	gtc	cgg	cgg	3664					
Ile	Asp	Gly	Ser	Leu	Tyr	Val	Gly	Asp	Phe	Asn	Tyr	Val	Arg	Arg						
1195										1200					1205					
ata	ttc	ccg	tct	ggg	aat	gtg	aca	agt	gtt	tta	gaa	cta	aga	aat	3709					
Ile	Phe	Pro	Ser	Gly	Asn	Val	Thr	Ser	Val	Leu	Glu	Leu	Arg	Asn						
1210										1215					1220					
aaa	gat	ttt	aga	cat	agt	agc	aac	cca	gct	cac	aga	tac	tac	ctg	3754					
Lys	Asp	Phe	Arg	His	Ser	Ser	Asn	Pro	Ala	His	Arg	Tyr	Tyr	Leu						
1225										1230					1235					
gct	acg	gac	cca	gtc	acc	gga	gat	ttg	tac	gtc	tct	gat	act	aac	3799					
Ala	Thr	Asp	Pro	Val	Thr	Gly	Asp	Leu	Tyr	Val	Ser	Asp	Thr	Asn						
1240										1245					1250					
acc	cgc	aga	atc	tat	cgg	ccg	aaa	tca	ctc	acg	gga	gcc	aaa	gac	3844					
Thr	Arg	Arg	Ile	Tyr	Arg	Pro	Lys	Ser	Leu	Thr	Gly	Ala	Lys	Asp						
1255										1260					1265					
ctg	act	aaa	aac	gct	gaa	gtg	gtg	gca	ggg	acc	ggg	gaa	cag	tgc	3889					

Leu	Thr	Lys	Asn	Ala	Glu	Val	Val	Ala	Gly	Thr	Gly	Glu	Gln	Cys	
				1270					1275					1280	
ctt	ccc	ttt	gac	gag	gcc	agg	tgt	ggg	gat	gga	ggc	aag	gct	gtg	3934
Leu	Pro	Phe	Asp	Glu	Ala	Arg	Cys	Gly	Asp	Gly	Gly	Lys	Ala	Val	
				1285					1290					1295	
gaa	gca	acg	ctc	atg	agt	ccc	aaa	gga	atg	gca	atc	gat	aag	aac	3979
Glu	Ala	Thr	Leu	Met	Ser	Pro	Lys	Gly	Met	Ala	Ile	Asp	Lys	Asn	
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gga	ctg	atc	tac	ttt	gtt	gat	gga	acc	atg	atc	aga	aag	gtt	gat	4024
Gly	Leu	Ile	Tyr	Phe	Val	Asp	Gly	Thr	Met	Ile	Arg	Lys	Val	Asp	
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caa	aat	gga	atc	ata	tca	act	ctc	ctg	ggc	tcc	aac	gac	ctc	acg	4069
Gln	Asn	Gly	Ile	Ile	Ser	Thr	Leu	Leu	Gly	Ser	Asn	Asp	Leu	Thr	
				1330					1335					1340	
tca	gct	cga	cct	tta	acc	tgt	gat	act	agc	atg	cat	atc	agc	cag	4114
Ser	Ala	Arg	Pro	Leu	Thr	Cys	Asp	Thr	Ser	Met	His	Ile	Ser	Gln	
				1345					1350					1355	
gtg	cgt	ctg	gaa	tgg	ccc	act	gac	ctc	gcg	atc	aac	ccc	atg	gat	4159
Val	Arg	Leu	Glu	Trp	Pro	Thr	Asp	Leu	Ala	Ile	Asn	Pro	Met	Asp	
				1360					1365					1370	
aac	tcc	atc	tac	gtc	ctg	gat	aat	aac	gta	gtt	tta	cag	atc	act	4204
Asn	Ser	Ile	Tyr	Val	Leu	Asp	Asn	Asn	Val	Val	Leu	Gln	Ile	Thr	
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gaa	aac	cgt	cag	gtc	cgc	atc	gct	gcc	ggg	cgg	ccc	atg	cac	tgt	4249
Glu	Asn	Arg	Gln	Val	Arg	Ile	Ala	Ala	Gly	Arg	Pro	Met	His	Cys	
				1390					1395					1400	
cag	gtc	cct	gga	gtg	gaa	tac	ccg	gtg	ggg	aag	cac	gcg	gtt	cag	4294
Gln	Val	Pro	Gly	Val	Glu	Tyr	Pro	Val	Gly	Lys	His	Ala	Val	Gln	
				1405					1410					1415	
acc	acc	ctg	gag	tca	gcc	acg	gcc	att	gct	gtg	tcc	tac	agc	ggg	4339
Thr	Thr	Leu	Glu	Ser	Ala	Thr	Ala	Ile	Ala	Val	Ser	Tyr	Ser	Gly	
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gtc	ctt	tac	atc	acg	gaa	act	gat	gag	aag	aag	atc	aac	cga	ata	4384
Val	Leu	Tyr	Ile	Thr	Glu	Thr	Asp	Glu	Lys	Lys	Ile	Asn	Arg	Ile	
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agg	cag	gtc	acg	aca	gac	ggg	gag	atc	tcc	tta	gtg	gct	ggg	ata	4429
Arg	Gln	Val	Thr	Thr	Asp	Gly	Glu	Ile	Ser	Leu	Val	Ala	Gly	Ile	
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cct	tcg	gaa	tgt	gac	tgc	aag	aac	gac	gcc	aac	tgt	gac	tgc	tac	4474
Pro	Ser	Glu	Cys	Asp	Cys	Lys	Asn	Asp	Ala	Asn	Cys	Asp	Cys	Tyr	
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caa	agc	gga	gac	ggc	tac	gcc	aaa	gat	gcc	aaa	ctc	aat	gcg	ccg	4519
Gln	Ser	Gly	Asp	Gly	Tyr	Ala	Lys	Asp	Ala	Lys	Leu	Asn	Ala	Pro	
				1480					1485					1490	

tcc tcc ctg gcc gcc	tcg cca gat ggc act	ctg tac att gca gat	4564
Ser Ser Leu Ala Ala	Ser Pro Asp Gly Thr	Leu Tyr Ile Ala Asp	
1495	1500	1505	
ctg gga aat atc agg	atc cgg gcc gtt tcg	aag aat aaa cct tta	4609
Leu Gly Asn Ile Arg	Ile Arg Ala Val Ser	Lys Asn Lys Pro Leu	
1510	1515	1520	
ctg aac tca atg aac	ttt tac gaa gtt gcc	tct cca act gat caa	4654
Leu Asn Ser Met Asn	Phe Tyr Glu Val Ala	Ser Pro Thr Asp Gln	
1525	1530	1535	
gag ctc tac atc ttt	gac atc aac ggt act	cac cag tac acc gtg	4699
Glu Leu Tyr Ile Phe	Asp Ile Asn Gly Thr	His Gln Tyr Thr Val	
1540	1545	1550	
agc ctg gtc acg ggt	gac tac cta tat aat	ttt agt tac agc aat	4744
Ser Leu Val Thr Gly	Asp Tyr Leu Tyr Asn	Phe Ser Tyr Ser Asn	
1555	1560	1565	
gac aat gac gtc acc	gct gta act gac agc	aat ggc aac acc ctc	4789
Asp Asn Asp Val Thr	Ala Val Thr Asp Ser	Asn Gly Asn Thr Leu	
1570	1575	1580	
cga atc cga agg gat	ccg aat cgg atg ccg	gtg cgg gtg gtg tct	4834
Arg Ile Arg Arg Asp	Pro Asn Arg Met Pro	Val Arg Val Val Ser	
1585	1590	1595	
cct gat aac cag gtg	ata tgg ttg acc ata	ggc acc aac ggg tgt	4879
Pro Asp Asn Gln Val	Ile Trp Leu Thr Ile	Gly Thr Asn Gly Cys	
1600	1605	1610	
ctg aaa agc atg acc	gct cag ggc ctg gaa	ctg gtt ttg ttt act	4924
Leu Lys Ser Met Thr	Ala Gln Gly Leu Glu	Leu Val Leu Phe Thr	
1615	1620	1625	
tac cat ggc aac agt	ggg ctt tta gcc acc	aaa agt gac gaa act	4969
Tyr His Gly Asn Ser	Gly Leu Leu Ala Thr	Lys Ser Asp Glu Thr	
1630	1635	1640	
gga tgg aca aca ttt	ttt gac tat gac agt	gaa ggt cgc ctg acg	5014
Gly Trp Thr Thr Phe	Phe Asp Tyr Asp Ser	Glu Gly Arg Leu Thr	
1645	1650	1655	
aat gtt acc ttc ccc	act ggg gtg gtt aca	aac ctg cac ggg gac	5059
Asn Val Thr Phe Pro	Thr Gly Val Val Thr	Asn Leu His Gly Asp	
1660	1665	1670	
atg gac aag gct atc	acg gtg gac atc gag	tca tcc agc aga gag	5104
Met Asp Lys Ala Ile	Thr Val Asp Ile Glu	Ser Ser Ser Arg Glu	
1675	1680	1685	
gaa gat gtc agc atc	act tcg aac ttg tcc	tcc atc gat tcc ttc	5149
Glu Asp Val Ser Ile	Thr Ser Asn Leu Ser	Ser Ile Asp Ser Phe	
1690	1695	1700	
tac acc atg gtc caa	gac cag tta aga aac	agt tac cag att ggg	5194
Tyr Thr Met Val Gln	Asp Gln Leu Arg Asn	Ser Tyr Gln Ile Gly	
1705	1710	1715	

tat gat ggc tcc ctt	aga atc ttc tat gcc	agt ggt ctg gac tct	5239
Tyr Asp Gly Ser Leu	Arg Ile Phe Tyr Ala	Ser Gly Leu Asp Ser	
1720	1725	1730	
cac tac cag aca gag	ccc cac gtt ctg gct	ggc acg gcg aat ccc	5284
His Tyr Gln Thr Glu	Pro His Val Leu Ala	Gly Thr Ala Asn Pro	
1735	1740	1745	
aca gta gcc aaa aga	aac atg act ctt ccc	ggt gag aac ggg cag	5329
Thr Val Ala Lys Arg	Asn Met Thr Leu Pro	Gly Glu Asn Gly Gln	
1750	1755	1760	
aat ctg gtg gag tgg	aga ttc cga aaa gaa	caa gcc cag ggc aaa	5374
Asn Leu Val Glu Trp	Arg Phe Arg Lys Glu	Gln Ala Gln Gly Lys	
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gtc aac gta ttc ggc	cgg aag ctc agg gtc	aat ggg cgc aac cta	5419
Val Asn Val Phe Gly	Arg Lys Leu Arg Val	Asn Gly Arg Asn Leu	
1780	1785	1790	
ctc tca gtg gac ttt	gat cgg acc acc aag	acg gaa aag atc tat	5464
Leu Ser Val Asp Phe	Asp Arg Thr Thr Lys	Thr Glu Lys Ile Tyr	
1795	1800	1805	
gat gac cac cgg aaa	ttt ctc ctg agg atc	gct tac gac acg tcg	5509
Asp Asp His Arg Lys	Phe Leu Leu Arg Ile	Ala Tyr Asp Thr Ser	
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ggg cac ccg act ctc	tgg ctg ccg agt agc	aag cta atg gca gtg	5554
Gly His Pro Thr Leu	Trp Leu Pro Ser Ser	Lys Leu Met Ala Val	
1825	1830	1835	
aac gtc acc tac tca	tcc acc ggt caa att	gcc agc atc cag aga	5599
Asn Val Thr Tyr Ser	Ser Thr Gly Gln Ile	Ala Ser Ile Gln Arg	
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ggg acc acg agc gaa	aag gtg gac tat gac	agc cag ggg agg atc	5644
Gly Thr Thr Ser Glu	Lys Val Asp Tyr Asp	Ser Gln Gly Arg Ile	
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gta tct cgg gtc ttt	gcc gat ggg aaa aca	tgg agt tac acg tac	5689
Val Ser Arg Val Phe	Ala Asp Gly Lys Thr	Trp Ser Tyr Thr Tyr	
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ttg gaa aag tcc atg	gtt ctt ctg ctc cat	agc cag cgg cag tac	5734
Leu Glu Lys Ser Met	Val Leu Leu Leu His	Ser Gln Arg Gln Tyr	
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Ile Phe Glu Tyr Asp	Met Trp Asp Arg Leu	Ser Ala Ile Thr Met	
1900	1905	1910	
ccc agt gtg gct cgc	cac acc atg cag acc	atc cgg tcc att ggc	5824
Pro Ser Val Ala Arg	His Thr Met Gln Thr	Ile Arg Ser Ile Gly	
1915	1920	1925	
tac tac cgc aac atc	tac aat ccc cca gaa	agc aat gcc tct atc	5869
Tyr Tyr Arg Asn Ile	Tyr Asn Pro Pro Glu	Ser Asn Ala Ser Ile	

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atc acc gac tac aac gag gaa ggg ctg ctt ctg caa aca gct ttc	1945	1950	1955	5914
Ile Thr Asp Tyr Asn Glu Glu Gly Leu Leu Leu Gln Thr Ala Phe				
ctg gga acg agt cgg agg gtc tta ttc aag tat aga agg cag acc	1960	1965	1970	5959
Leu Gly Thr Ser Arg Arg Val Leu Phe Lys Tyr Arg Arg Gln Thr				
agg cta tca gaa att tta tac gac agc aca aga gtc agt ttt acc	1975	1980	1985	6004
Arg Leu Ser Glu Ile Leu Tyr Asp Ser Thr Arg Val Ser Phe Thr				
tac gac gaa aca gcg gga gtc ctg aaa aca gta aac ctt cag agt	1990	1995	2000	6049
Tyr Asp Glu Thr Ala Gly Val Leu Lys Thr Val Asn Leu Gln Ser				
gat ggt ttt att tgc acc att aga tac agg caa att ggt ccc ctg	2005	2010	2015	6094
Asp Gly Phe Ile Cys Thr Ile Arg Tyr Arg Gln Ile Gly Pro Leu				
att gac aga cag att ttc cgc ttc agc gag gat gga atg gta aat	2020	2025	2030	6139
Ile Asp Arg Gln Ile Phe Arg Phe Ser Glu Asp Gly Met Val Asn				
gcg aga ttt gac tat agc tac gac aac agc ttt cga gtg acc agc	2035	2040	2045	6184
Ala Arg Phe Asp Tyr Ser Tyr Asp Asn Ser Phe Arg Val Thr Ser				
atg cag ggt gtc atc aat gaa aca cca ctg ccc att gat cta tac	2050	2055	2060	6229
Met Gln Gly Val Ile Asn Glu Thr Pro Leu Pro Ile Asp Leu Tyr				
cag ttt gat gac atc tct ggc aaa gtc gag cag ttt gga aaa ttc	2065	2070	2075	6274
Gln Phe Asp Asp Ile Ser Gly Lys Val Glu Gln Phe Gly Lys Phe				
gga gtg ata tac tac gac atc aac caa atc att tcc acg gcc gtg	2080	2085	2090	6319
Gly Val Ile Tyr Tyr Asp Ile Asn Gln Ile Ile Ser Thr Ala Val				
atg act tat aca aag cac ttt gat gct cat ggg cgc atc aag gag	2095	2100	2105	6364
Met Thr Tyr Thr Lys His Phe Asp Ala His Gly Arg Ile Lys Glu				
atc caa tat gag ata ttt agg tca ctc atg tac tgg att aca att	2110	2115	2120	6409
Ile Gln Tyr Glu Ile Phe Arg Ser Leu Met Tyr Trp Ile Thr Ile				
caa tat gat aat atg ggc cgg gta acc aag aga gag att aaa att	2125	2130	2135	6454
Gln Tyr Asp Asn Met Gly Arg Val Thr Lys Arg Glu Ile Lys Ile				
ggg cct ttt gcc aac act acc aaa tac gcg tac gag tac gac gtc	2140	2145	2150	6499
Gly Pro Phe Ala Asn Thr Thr Lys Tyr Ala Tyr Glu Tyr Asp Val				
gat gga cag ctc caa aca gtt tac cta aac gaa aag atc atg tgg				6544

Asp Gly Gln Leu Gln Thr Val Tyr Leu Asn Glu Lys Ile Met Trp	
2155 2160 2165	
cgg tac aac tac gac cta aat gga aac ctc cac ttg ctc aac ccc	6589
Arg Tyr Asn Tyr Asp Leu Asn Gly Asn Leu His Leu Leu Asn Pro	
2170 2175 2180	
agc agc agc gcc cgc ctg acc cct ctg cgc tat gac ctg cgc gac	6634
Ser Ser Ser Ala Arg Leu Thr Pro Leu Arg Tyr Asp Leu Arg Asp	
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aga atc acc cgc ctg ggc gat gtt cag tac cgg ctg gat gaa gat	6679
Arg Ile Thr Arg Leu Gly Asp Val Gln Tyr Arg Leu Asp Glu Asp	
2200 2205 2210	
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Gly Phe Leu Arg Gln Arg Gly Thr Glu Ile Phe Glu Tyr Ser Ser	
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Lys Gly Leu Leu Thr Arg Val Tyr Ser Lys Gly Ser Gly Trp Thr	
2230 2235 2240	
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Val Ile Tyr Arg Tyr Asp Gly Leu Gly Arg Arg Val Ser Ser Lys	
2245 2250 2255	
acc agc ctg gga cag cac ctt cag ttt ttc tac gcc gac ctg aca	6859
Thr Ser Leu Gly Gln His Leu Gln Phe Phe Tyr Ala Asp Leu Thr	
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Tyr Pro Thr Arg Ile Thr His Val Tyr Asn His Ser Ser Ser Glu	
2275 2280 2285	
atc acc tcc ctg tac tat gac ctc caa gga cat ctc ttc gcc atg	6949
Ile Thr Ser Leu Tyr Tyr Asp Leu Gln Gly His Leu Phe Ala Met	
2290 2295 2300	
gag atc agc agt ggg gat gag ttc tac atc gcc tcg gac aac acg	6994
Glu Ile Ser Ser Gly Asp Glu Phe Tyr Ile Ala Ser Asp Asn Thr	
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Gly Thr Pro Leu Ala Val Phe Ser Ser Asn Gly Leu Met Leu Lys	
2320 2325 2330	
cag acc cag tac act gcc tat ggt gag atc tac ttt gac tcc aac	7084
Gln Thr Gln Tyr Thr Ala Tyr Gly Glu Ile Tyr Phe Asp Ser Asn	
2335 2340 2345	
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Val Asp Phe Gln Leu Val Ile Gly Phe His Gly Gly Leu Tyr Asp	
2350 2355 2360	
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Pro Leu Thr Lys Leu Ile His Phe Gly Glu Arg Asp Tyr Asp Ile	
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Ile Gly Lys Asp Pro Ala Pro Phe Asn Leu Tyr Met Phe Arg Asn	
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Asp Val Asn Ser Trp Leu Val Thr Phe Gly Phe His Leu His Asn	
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Ser Tyr Glu Leu Val Lys Ser Gln Gln Trp Glu Asp Val Pro Pro	
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Leu Ile Gly Lys Gly Val Met Leu Ala Val Ser Gln Gly Arg Val	
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Gln Thr Asn Val Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val	
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Thr Ile Glu Gly Lys Asp Thr His Tyr Phe Ile Lys Thr Thr Thr	
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ccc gag agc gac ctg ggc aca ctg cgg ctg acg agc ggt cgc aag	7804
Pro Glu Ser Asp Leu Gly Thr Leu Arg Leu Thr Ser Gly Arg Lys	
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gcc ctg gag aac ggg atc aac gtg acc gtg tct cag tcc acc acg	7849
Ala Leu Glu Asn Gly Ile Asn Val Thr Val Ser Gln Ser Thr Thr	
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gtg gtg aac ggc agg act cgc agg ttc gcc gac gtg gag atg cag	7894
Val Val Asn Gly Arg Thr Arg Arg Phe Ala Asp Val Glu Met Gln	
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ttc ggt gcc ctg gca ctg cat gtg cgc tat ggc atg acg ctg gac	7939
Phe Gly Ala Leu Ala Leu His Val Arg Tyr Gly Met Thr Leu Asp	
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Glu Glu Lys Ala Arg Ile Leu Glu Gln Ala Arg Gln Arg Ala Leu	
2635 2640 2645	
gcc cgg gcg tgg gca cgg gag cag cag cgc gtg cgc gac ggc gag	8029
Ala Arg Ala Trp Ala Arg Glu Gln Gln Arg Val Arg Asp Gly Glu	
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Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val Leu Ser	
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Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile Gln	
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Met Tyr Ser
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Val Asp Arg Val Ser Asp Ile Pro Ile Arg Thr Trp Phe Pro Lys
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Phe Arg Gly Tyr Ala Glu Arg Lys Arg Lys Arg Glu Asn Asp Ser
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gcg tct gta atc cag agg aac ttc cgc aaa cac ctg cgc atg gtc ggc 307
Ala Ser Val Ile Gln Arg Asn Phe Arg Lys His Leu Arg Met Val Gly
55 60 65

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Ser Arg Arg Val Lys Ala Gln Thr Phe Ala Glu Arg Arg Glu Arg Ser
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			20					25					30		

Gln	Asn	Glu	Met
		35	